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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/700,816	11/04/2003	Zuoshang Xu	UMY-038	9864
959	7590	10/05/2006	EXAMINER	
LAHIVE & COCKFIELD 28 STATE STREET BOSTON, MA 02109			MCGARRY, SEAN	
			ART UNIT	PAPER NUMBER
			1635	

DATE MAILED: 10/05/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Response to Amendment

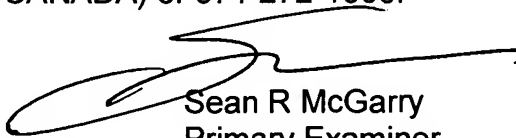
The reply filed on 7/10/06 is not fully responsive to the prior Office Action because of the following omission(s) or matter(s): In response to the restriction requirement mailed 6/08/06, applicant filed an amendment/correction to the CRF of the sequence listing. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application now fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sean R. McGarry whose telephone number is (571) 272-0761. The examiner can normally be reached on M-Th (6:00-4:30).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Peter Paras can be reached on (571) 272-4517. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.



Sean R McGarry
Primary Examiner
Art Unit 1635

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicants attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a Sequence Listing as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the Sequence Listing in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the Sequence Listing in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, **as indicated on the attached copy of the marked-up Raw Sequence Listing.**
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the Sequence Listing is not the same as the computer readable from of the Sequence Listing as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the Sequence Listing. (If the unidentified sequences are not provided on the CRF)
- ☒ An initial or substitute paper copy of the Sequence Listing, as well as an amendment directing its entry into the specification. (If the unidentified sequences are not provided in the paper copy)
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d). (If a new paper and/or CRF are required)

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/700,816A
Source: IFW16
Date Processed by STIC: 7/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/700, 816A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 ____ Use of <220>	Sequence(s) <u>16</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,816A

DATE: 07/14/2006
TIME: 09:11:02

Input Set : A:\new SEQLIST txt.txt
Output Set: N:\CRF4\07142006\J700816A.raw

4 <110> APPLICANT: Xu, Zuoshang and Zamore, Phillip D.
6 <120> TITLE OF INVENTION: Allele-Specific RNA Interference
9 <130> FILE REFERENCE: UMY-038
11 <140> CURRENT APPLICATION NUMBER: 10/700816A
12 <141> CURRENT FILING DATE: 2003-11-04
14 <150> PRIOR APPLICATION NUMBER: 60/423,507
15 <151> PRIOR FILING DATE: 2002-11-04
17 <150> PRIOR APPLICATION NUMBER: 60/488,283
18 <151> PRIOR FILING DATE: 2003-07-18
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0

see p 2-3, 5

**Does Not Comply
Corrected Diskette Needed**

ERRORRED SEQUENCES

280 <210> SEQ ID NO: 19
281 <211> LENGTH: 2288
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 19

P.2

286 gtaccctggt tacatcattt tgccattttc gcgtactgca accggcgggc cagcccggtga	60
287 aaagaagggt gttttctcca cagtttcggg gttctggacg tttcccggtc gcggggcggg	120
288 gggagttctc ggcgcacgcg gccccttggc ccgccccagt cattcccggc cactcgcgac	180
289 ccgaggtctc cgcagggggc gggctgagcg cgtgcgaggc cattggtttg gggccagagt	240
290 gggcgaggcg cggaggtctg gcctataaag tagtcgcgga gacggggtgc tggtttgctg	300
291 cgtagtctcc tgcaggtctg gggtttcctg tgcagtcctc ggaaccagga cctcggcgtg	360
292 gcctagcagag ttatggcgac gaaggccgtg tgcgtgctga agggcgacgg cccagtgcag	420
293 ggcacatcat atttcgagca gaaggcaagg gctgggaccg ggaggcttgt gttgcgaggc	480
294 cgctcccgac ccgctcgtcc ccccgcgacc ctttgcattg acgggtcgcc cgccagggtc	540
295 agagcagtta agcagcttgc tggagggttca ctgggtagaa agtggtcagc ctgggattgc	600
296 atggacggat ttttccactc ccaagtctgg ctgcttttta cttcactgtg aggggtaaag	660
297 gtaaatacagc tgttttcttt gtccagaaac tctctccaac tttgcacttt tcttaaagga	720
298 aagtaatgga ccagtgaagg tgtggggaag cattaagga ctgactgaag gcctgcatgg	780
299 attccatggt catgagtttg gagataatac agcaggtggg tcataattta gctttttttt	840
300 cttctttctta taaataggct gtaccagtgc aggtcctcac tttaatcctc tatccagaaa	900
301 acacgggtgg ccaaaggatg aagagaggta acaagatgct taactcttgt aatcaatggc	960
302 gatacgtttc tggagttcat atggtatact acttgtaaat atgtgcctaa gataattccg	1020
303 tgtttccccc acctttgctt ttgaacttgc tgactcatgt gaaaccctgc tcccaaattg	1080
304 tggaaatgctt ttacttctcg ggcttaaaag aattgacaaa tgggcactta aaacgatttg	1140
305 gttttgtagc atttgattga atatagaact aatacaagt ccaaagggga actaatacag	1200
306 gaaatgttca tgaacagtac tgtcaaccac tagcaaaatc aatcatcatt tgatgctttt	1260
307 catataggca tgttgagac ttgggcaatg tgactgctga caaagatggg gtggccgatg	1320
308 tgtctattga agattctgtg atctcactct caggagacca ttgcatcatt ggccgcacac	1380

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/700,816A

DATE: 07/14/2006

TIME: 09:11:02

Input Set : A:\new SEQLIST txt.txt

Output Set: N:\CRF4\07142006\J700816A.raw

```
309 tgggtggaag ttttcataaa ggatatgcat aaaacttctt ctaacagtac agtcatgtat 1440
310 ctttcacttt gattgttagt cgcggaattct aagatccaga taaactgtgt ttctgctttt 1500
311 aaactactaa atattagtat atctctctac taggattaat gttatttttc taatattatg 1560
312 aggttcctta acatcttttg ggtattgttg ggaggaggta gtgattactt gacagcccaa 1620
313 agttatcttc ttaaaatttt ttacagggtc atgaaaaagc agatgacttg ggcaaagggtg 1680
314 gaaatgaaga aagtacaaag acaggaaacg ctggaagtcg tttggcttgt ggtgtaattg 1740
315 ggatcgccca ataaacattc ccttggaagt agtctgaggg cccttaactc atctgttatc 1800
316 ctgctagctg tagaaatgta tcttgataaa cattaaacac tgtaatctta aaagtgtaat 1860
317 tgtgtgactt tttcagagtt gcttttaaagt acctgtagtg agaaactgat ttatgatcac 1920
318 ttggaagatt tgtatagttt tataaaactc agttaaagt tctgtttcaa tgacctgtat 1980
319 tttgccagac ttaaatcaca gatgggtatt aaacttgtca gaatttcttt gtcattcaag 2040
320 cctgtgaata aaaaccctgt atggcactta ttatgaggct attaaaagaa tccaaattca 2100
321 aactaaatta gctctgatac ttatttatat aaacagcttc agtggaacag atttagtaat 2160
322 actaacagtg atagcatttt attttgaaag tgttttgaga ccatcaaaat gcatacttta 2220
323 aaacagcagg tcttttagct aaaactaaca caactctgct tagacaaata ggctgtcctt 2280
324 tgaagctt 2288
```

E--> 325 umy-038

E--> 330 1

delete

10/700, 8/6A

3

<210> 1
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> synthetic

<221> misc_feature
<222> 20, 21
<223> n-deoxy thymidine

<400> 1
uggagacuug cgcaaugugn n

It's not allowed in an RNA sequence, even if they're represented by n's

same error in seqs. 2-6, 9-14

21
for a combined DNA/RNA sequence, use <212> DNA and explain in <220>-<223> section

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/700,816A

DATE: 07/14/2006

TIME: 09:11:03

Input Set : A:\new SEQLIST txt.txt

Output Set: N:\CRF4\07142006\J700816A.raw

L:32 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
 L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
 L:47 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
 L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
 L:62 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
 L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:78 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
 L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
 L:93 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:97 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
 L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
 L:108 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
 L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
 L:139 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
 L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
 L:154 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
 L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
 L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
 L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
 L:184 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
 L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
 L:199 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
 L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
 L:214 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:218 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
 L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
 L:234 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
 ORGANISM:Artificial Sequence
 L:234 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
 ORGANISM:Artificial Sequence
 L:234 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:234
 L:325 M:254 E: No. of Bases conflict, LENGTH:Input:-38 Counted:2292 SEQ:19
 L:325 M:112 C: (48) String data converted to lower case,
 M:254 Repeated in SeqNo=19
 L:330 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2288 Found:2292 SEQ:19

10/700, 8/6A 5

<210> 16

<211> 52

<212> RNA

<213> Artificial Sequence

<400> 16

gacaaagaug cuguggccga uaagcuuaucc ggccacagca ucuuugucuu uu

52

see item 11 on Ena summary sheet